



Amot/D

SEQUENCE LISTING

<110> Dessen, Andrea
Somers, William S.
Stahl, Mark L.
Seehra, Jasbir S.

<120> CRYSTAL STRUCTURE OF cPLA2, AND METHODS OF IDENTIFYING
AGONISTS AND ANTAGONISTS USING SAME

<130> GFN-5341

<140> 09/250,083

<141> 1999-02-15

<160> 3

<170> PatentIn Ver. 2.0

<210> 1

<211> 2247

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2247)

<400> 1

atg tca ttt ata gat cct tac cag cac att ata gtg gag cac cag tat	48
Met Ser Phe Ile Asp Pro Tyr Gln His Ile Ile Val Glu His Gln Tyr	
1 5 10 15	
tcc cac aag ttt acg gta gtg gtg tta cgt gcc acc aaa gtg aca aag	96
Ser His Lys Phe Thr Val Val Val Leu Arg Ala Thr Lys Val Thr Lys	
20 25 30	
ggg gcc ttt ggt gac atg ctt gat act cca gat ccc tat gtg gaa ctt	144
Gly Ala Phe Gly Asp Met Leu Asp Thr Pro Asp Pro Tyr Val Glu Leu	
35 40 45	
ttt atc tct aca acc cct gac agc agg aag aga aca aga cat ttc aat	192
Phe Ile Ser Thr Thr Pro Asp Ser Arg Lys Arg Thr Arg His Phe Asn	
50 55 60	
aat gac ata aac cct gtg tgg aat gag acc ttt gaa ttt att ttg gat	240
Asn Asp Ile Asn Pro Val Trp Asn Glu Thr Phe Glu Phe Ile Leu Asp	
65 70 75 80	
cct aat cag gaa aat gtt ttg gag att acg tta atg gat gcc aat tat	288
Pro Asn Gln Glu Asn Val Leu Glu Ile Thr Leu Met Asp Ala Asn Tyr	
85 90 95	
gtc atg gat gaa act cta ggg aca gca aca ttt act gta tct tct atg	336
Val Met Asp Glu Thr Leu Gly Thr Ala Thr Phe Thr Val Ser Ser Met	
100 105 110	
aag gtg gga gaa aag aaa gaa gtt cct ttt att ttc aac caa gtc act	384
Lys Val Gly Glu Lys Lys Glu Val Pro Phe Ile Phe Asn Gln Val Thr	
115 120 125	

RECEIVED

JAN 22 2003

TECH CENTER 1600/2900

gaa atg gtt cta gaa atg tct ctt gaa gtt tgc tca tgc cca gac cta	432
Glu Met Val Leu Glu Met Ser Leu Glu Val Cys Ser Cys Pro Asp Leu	
130 135 140	
cga ttt agt atg gct ctg tgt gat cag gag aag act ttc aga caa cag	480
Arg Phe Ser Met Ala Leu Cys Asp Gln Glu Lys Thr Phe Arg Gln Gln	
145 150 155 160	
aga aaa gaa cac ata agg gag agc atg aag aaa ctc ttg ggt cca aag	528
Arg Lys Glu His Ile Arg Glu Ser Met Lys Lys Leu Leu Gly Pro Lys	
165 170 175	
aat agt gaa gga ttg cat tct gca cgt gat gtg cct gtg gta gcc ata	576
Asn Ser Glu Gly Leu His Ser Ala Arg Asp Val Pro Val Val Ala Ile	
180 185 190	
ttg ggt tca ggt ggg ggt ttc cga gcc atg gtg gga ttc tct ggt gtg	624
Leu Gly Ser Gly Gly Gly Phe Arg Ala Met Val Gly Phe Ser Gly Val	
195 200 205	
atg aag gca tta tac gaa tca gga att ctg gat tgt gct acc tac gtt	672
Met Lys Ala Leu Tyr Glu Ser Gly Ile Leu Asp Cys Ala Thr Tyr Val	
210 215 220	
gct ggt ctt tct ggc tcc acc tgg tat atg tca acc ttg tat tct cac	720
Ala Gly Leu Ser Gly Ser Thr Trp Tyr Met Ser Thr Leu Tyr Ser His	
225 230 235 240	
cct gat ttt cca gag aaa ggg cca gag gag att aat gaa gaa cta atg	768
Pro Asp Phe Pro Glu Lys Gly Pro Glu Glu Ile Asn Glu Glu Leu Met	
245 250 255	
aaa aat gtt agc cac aat ccc ctt tta ctt ctc aca cca cag aaa gtt	816
Lys Asn Val Ser His Asn Pro Leu Leu Leu Thr Pro Gln Lys Val	
260 265 270	
aaa aga tat gtt gag tct tta tgg aag aag aaa agc tct gga caa cct	864
Lys Arg Tyr Val Glu Ser Leu Trp Lys Lys Lys Ser Ser Gly Gln Pro	
275 280 285	
gtc acc ttt act gat atc ttt ggg atg tta ata gga gaa aca cta att	912
Val Thr Phe Thr Asp Ile Phe Gly Met Leu Ile Gly Glu Thr Leu Ile	
290 295 300	
cat aat aga atg aat act act ctg agc agt ttg aag gaa aaa gtt aat	960
His Asn Arg Met Asn Thr Thr Leu Ser Ser Leu Lys Glu Lys Val Asn	
305 310 315 320	
act gca caa tgc cct tta cct ctt ttc acc tgt ctt cat gtc aaa cct	1008
Thr Ala Gln Cys Pro Leu Pro Leu Phe Thr Cys Leu His Val Lys Pro	
325 330 335	
gac gtt tca gag ctg atg ttt gca gat tgg gtt gaa ttt agt cca tac	1056
Asp Val Ser Glu Leu Met Phe Ala Asp Trp Val Glu Phe Ser Pro Tyr	
340 345 350	
gaa att ggc atg gct aaa tat ggt act ttt atg gct ccc gac tta ttt	1104
Glu Ile Gly Met Ala Lys Tyr Gly Thr Phe Met Ala Pro Asp Leu Phe	
355 360 365	
gga agc aaa ttt ttt atg gga aca gtc gtt aag aag tat gaa gaa aac	1152

Gly	Ser	Lys	Phe	Phe	Met	Gly	Thr	Val	Val	Lys	Lys	Tyr	Glu	Glu	Asn		
370						375					380						
ccc	ttg	cat	ttc	tta	atg	ggt	gtc	tgg	ggc	agt	gcc	ttt	tcc	ata	ttg	1200	
Pro	Leu	His	Phe	Leu	Met	Gly	Val	Trp	Gly	Ser	Ala	Phe	Ser	Ile	Leu	385	400
					390					395							
ttc	aac	aga	gtt	ttg	ggc	gtt	tct	ggt	tca	caa	agc	aga	ggc	tcc	aca	1248	
Phe	Asn	Arg	Val	Leu	Gly	Val	Ser	Gly	Ser	Gln	Ser	Arg	Gly	Ser	Thr	405	415
				405				410									
atg	gag	gaa	gaa	tta	gaa	aat	att	acc	aca	aag	cat	att	gtg	agt	aat	1296	
Met	Glu	Glu	Glu	Leu	Glu	Asn	Ile	Thr	Thr	Lys	His	Ile	Val	Ser	Asn	420	430
				420				425									
gat	agc	tcg	gac	agt	gat	gat	gaa	tca	cac	gaa	ccc	aaa	ggc	act	gaa	1344	
Asp	Ser	Ser	Asp	Ser	Asp	Asp	Glu	Ser	His	Glu	Pro	Lys	Gly	Thr	Glu	435	445
							440										
aat	gaa	gat	gct	gga	agt	gac	tat	caa	agt	gat	aat	caa	gca	agt	tgg	1392	
Asn	Glu	Asp	Ala	Gly	Ser	Asp	Tyr	Gln	Ser	Asp	Asn	Gln	Ala	Ser	Trp	450	460
						455											
att	cat	cgt	atg	ata	atg	gcc	ttg	gtg	agt	gat	tca	gct	tta	ttc	aat	1440	
Ile	His	Arg	Met	Ile	Met	Ala	Leu	Val	Ser	Asp	Ser	Ala	Leu	Phe	Asn	465	480
					470					475							
acc	aga	gaa	gga	cgt	gct	ggg	aag	gta	cac	aac	ttc	atg	ctg	ggc	ttg	1488	
Thr	Arg	Glu	Gly	Arg	Ala	Gly	Lys	Val	His	Asn	Phe	Met	Leu	Gly	Leu	485	495
				485				490									
aat	ctc	aat	aca	tct	tat	cca	ctg	tct	cct	ttg	agt	gac	ttt	gcc	aca	1536	
Asn	Leu	Asn	Thr	Ser	Tyr	Pro	Leu	Ser	Pro	Leu	Ser	Asp	Phe	Ala	Thr	500	510
							505										
cag	gac	tcc	ttt	gat	gat	gat	gaa	ctg	gat	gca	gct	gta	gca	gat	cct	1584	
Gln	Asp	Ser	Phe	Asp	Asp	Asp	Glu	Leu	Asp	Ala	Ala	Val	Ala	Asp	Pro	515	525
							520										
gat	gaa	ttt	gag	cga	ata	tat	gag	cct	ctg	gat	gtc	aaa	agt	aaa	aag	1632	
Asp	Glu	Phe	Glu	Arg	Ile	Tyr	Glu	Pro	Leu	Asp	Val	Lys	Ser	Lys	Lys	530	540
						535											
att	cat	gta	gtg	gac	agt	ggg	ctc	aca	ttt	aac	ctg	ccg	tat	ccc	ttg	1680	
Ile	His	Val	Val	Asp	Ser	Gly	Leu	Thr	Phe	Asn	Leu	Pro	Tyr	Pro	Leu	545	560
					550					555							
ata	ctg	aga	cct	cag	aga	ggg	gtt	gat	ctc	ata	atc	tcc	ttt	gac	ttt	1728	
Ile	Leu	Arg	Pro	Gln	Arg	Gly	Val	Asp	Leu	Ile	Ile	Ser	Phe	Asp	Phe	565	575
									570								
tct	gca	agg	cca	agt	gac	tct	agt	cct	ccg	ttc	aag	gaa	ctt	cta	ctt	1776	
Ser	Ala	Arg	Pro	Ser	Asp	Ser	Ser	Pro	Pro	Phe	Lys	Glu	Leu	Leu	Leu	580	590
								585									
gca	gaa	aag	tgg	gct	aaa	atg	aac	aag	ctc	ccc	ttt	cca	aag	att	gat	1824	
Ala	Glu	Lys	Trp	Ala	Lys	Met	Asn	Lys	Leu	Pro	Phe	Pro	Lys	Ile	Asp	595	605
						600											
cct	tat	gtg	ttt	gat	cgg	gaa	ggg	ctg	aag	gag	tgc	tat	gtc	ttt	aaa	1872	
Pro	Tyr	Val	Phe	Asp	Arg	Glu	Gly	Leu	Lys	Glu	Cys	Tyr	Val	Phe	Lys		

610	615	620	
ccc aag aat cct gat atg gag aaa gat tgc cca acc atc atc cac ttt			1920
Pro Lys Asn Pro Asp Met Glu Lys Asp Cys Pro Thr Ile Ile His Phe			
625	630	635	640
ggt ctg gcc aac atc aac ttc aga aag tac aag gct cca ggt gtt cca			1968
Val Leu Ala Asn Ile Asn Phe Arg Lys Tyr Lys Ala Pro Gly Val Pro			
	645	650	655
agg gaa act gag gaa gag aaa gaa atc gct gac ttt gat att ttt gat			2016
Arg Glu Thr Glu Glu Glu Lys Glu Ile Ala Asp Phe Asp Ile Phe Asp			
	660	665	670
gac cca gaa tca cca ttt tca acc ttc aat ttt caa tat cca aat caa			2064
Asp Pro Glu Ser Pro Phe Ser Thr Phe Asn Phe Gln Tyr Pro Asn Gln			
	675	680	685
gca ttc aaa aga cta cat gat ctt atg cac ttc aat act ctg aac aac			2112
Ala Phe Lys Arg Leu His Asp Leu Met His Phe Asn Thr Leu Asn Asn			
	690	695	700
att gat gtg ata aaa gaa gcc atg gtt gaa agc att gaa tat aga aga			2160
Ile Asp Val Ile Lys Glu Ala Met Val Glu Ser Ile Glu Tyr Arg Arg			
	705	710	720
cag aat cca tct cgt tgc tct gtt tcc ctt agt aat gtt gag gca aga			2208
Gln Asn Pro Ser Arg Cys Ser Val Ser Leu Ser Asn Val Glu Ala Arg			
	725	730	735
aga ttt ttc aac aag gag ttt cta agt aaa ccc aaa gca			2247
Arg Phe Phe Asn Lys Glu Phe Leu Ser Lys Pro Lys Ala			
	740	745	

<210> 2

<211> 749

<212> PRT

<213> Homo sapiens

<400> 2

Met Ser Phe Ile Asp Pro Tyr Gln His Ile Ile Val Glu His Gln Tyr	
1 5 10 15	
Ser His Lys Phe Thr Val Val Val Leu Arg Ala Thr Lys Val Thr Lys	
20 25 30	
Gly Ala Phe Gly Asp Met Leu Asp Thr Pro Asp Pro Tyr Val Glu Leu	
35 40 45	
Phe Ile Ser Thr Thr Pro Asp Ser Arg Lys Arg Thr Arg His Phe Asn	
50 55 60	
Asn Asp Ile Asn Pro Val Trp Asn Glu Thr Phe Glu Phe Ile Leu Asp	
65 70 75 80	
Pro Asn Gln Glu Asn Val Leu Glu Ile Thr Leu Met Asp Ala Asn Tyr	
85 90 95	
Val Met Asp Glu Thr Leu Gly Thr Ala Thr Phe Thr Val Ser Ser Met	
100 105 110	

Lys Val Gly Glu Lys Lys Glu Val Pro Phe Ile Phe Asn Gln Val Thr
 115 120 125
 Glu Met Val Leu Glu Met Ser Leu Glu Val Cys Ser Cys Pro Asp Leu
 130 135 140
 Arg Phe Ser Met Ala Leu Cys Asp Gln Glu Lys Thr Phe Arg Gln Gln
 145 150 155 160
 Arg Lys Glu His Ile Arg Glu Ser Met Lys Lys Leu Leu Gly Pro Lys
 165 170 175
 Asn Ser Glu Gly Leu His Ser Ala Arg Asp Val Pro Val Val Ala Ile
 180 185 190
 Leu Gly Ser Gly Gly Gly Phe Arg Ala Met Val Gly Phe Ser Gly Val
 195 200 205
 Met Lys Ala Leu Tyr Glu Ser Gly Ile Leu Asp Cys Ala Thr Tyr Val
 210 215 220
 Ala Gly Leu Ser Gly Ser Thr Trp Tyr Met Ser Thr Leu Tyr Ser His
 225 230 235 240
 Pro Asp Phe Pro Glu Lys Gly Pro Glu Glu Ile Asn Glu Glu Leu Met
 245 250 255
 Lys Asn Val Ser His Asn Pro Leu Leu Leu Leu Thr Pro Gln Lys Val
 260 265 270
 Lys Arg Tyr Val Glu Ser Leu Trp Lys Lys Lys Ser Ser Gly Gln Pro
 275 280 285
 Val Thr Phe Thr Asp Ile Phe Gly Met Leu Ile Gly Glu Thr Leu Ile
 290 295 300
 His Asn Arg Met Asn Thr Thr Leu Ser Ser Leu Lys Glu Lys Val Asn
 305 310 315 320
 Thr Ala Gln Cys Pro Leu Pro Leu Phe Thr Cys Leu His Val Lys Pro
 325 330 335
 Asp Val Ser Glu Leu Met Phe Ala Asp Trp Val Glu Phe Ser Pro Tyr
 340 345 350
 Glu Ile Gly Met Ala Lys Tyr Gly Thr Phe Met Ala Pro Asp Leu Phe
 355 360 365
 Gly Ser Lys Phe Phe Met Gly Thr Val Val Lys Lys Tyr Glu Glu Asn
 370 375 380
 Pro Leu His Phe Leu Met Gly Val Trp Gly Ser Ala Phe Ser Ile Leu
 385 390 395 400
 Phe Asn Arg Val Leu Gly Val Ser Gly Ser Gln Ser Arg Gly Ser Thr
 405 410 415
 Met Glu Glu Glu Leu Glu Asn Ile Thr Thr Lys His Ile Val Ser Asn
 420 425 430

Asp Ser Ser Asp Ser Asp Asp Glu Ser His Glu Pro Lys Gly Thr Glu
 435 440 445
 Asn Glu Asp Ala Gly Ser Asp Tyr Gln Ser Asp Asn Gln Ala Ser Trp
 450 455 460
 Ile His Arg Met Ile Met Ala Leu Val Ser Asp Ser Ala Leu Phe Asn
 465 470 475 480
 Thr Arg Glu Gly Arg Ala Gly Lys Val His Asn Phe Met Leu Gly Leu
 485 490 495
 Asn Leu Asn Thr Ser Tyr Pro Leu Ser Pro Leu Ser Asp Phe Ala Thr
 500 505 510
 Gln Asp Ser Phe Asp Asp Asp Glu Leu Asp Ala Ala Val Ala Asp Pro
 515 520 525
 Asp Glu Phe Glu Arg Ile Tyr Glu Pro Leu Asp Val Lys Ser Lys Lys
 530 535 540
 Ile His Val Val Asp Ser Gly Leu Thr Phe Asn Leu Pro Tyr Pro Leu
 545 550 555 560
 Ile Leu Arg Pro Gln Arg Gly Val Asp Leu Ile Ile Ser Phe Asp Phe
 565 570 575
 Ser Ala Arg Pro Ser Asp Ser Ser Pro Pro Phe Lys Glu Leu Leu Leu
 580 585 590
 Ala Glu Lys Trp Ala Lys Met Asn Lys Leu Pro Phe Pro Lys Ile Asp
 595 600 605
 Pro Tyr Val Phe Asp Arg Glu Gly Leu Lys Glu Cys Tyr Val Phe Lys
 610 615 620
 Pro Lys Asn Pro Asp Met Glu Lys Asp Cys Pro Thr Ile Ile His Phe
 625 630 635 640
 Val Leu Ala Asn Ile Asn Phe Arg Lys Tyr Lys Ala Pro Gly Val Pro
 645 650 655
 Arg Glu Thr Glu Glu Glu Lys Glu Ile Ala Asp Phe Asp Ile Phe Asp
 660 665 670
 Asp Pro Glu Ser Pro Phe Ser Thr Phe Asn Phe Gln Tyr Pro Asn Gln
 675 680 685
 Ala Phe Lys Arg Leu His Asp Leu Met His Phe Asn Thr Leu Asn Asn
 690 695 700
 Ile Asp Val Ile Lys Glu Ala Met Val Glu Ser Ile Glu Tyr Arg Arg
 705 710 715 720
 Gln Asn Pro Ser Arg Cys Ser Val Ser Leu Ser Asn Val Glu Ala Arg
 725 730 735
 Arg Phe Phe Asn Lys Glu Phe Leu Ser Lys Pro Lys Ala
 740 745

<210> 3

<211> 5

<212> PRT

<213> Homo sapiens

<400> 3

Gly Leu Ser Gly Ser
1 5